FIGURE 1A

```
            *** *           *          *     *   ***
SEQ ID NO:10   -----TYCDLRSNNNKEQSREVKNN--------FTEPTRPQIKNKMSSSNSKTKTPSS
SEQ ID NO:18   MAAAMAATTMVTKNNRASLVMDKKNWLLRPVPEVAFPWSSQPESRS-LDFPRRALFASVG
SEQ ID NO:21   MAATMAVTTMVTRS-------KESWSSLQVPAVAFPWKPRGGKTGGLEFPRRAMFASVG
               1                                                       60

            *             *                                    *
SEQ ID NO:10   LSLCNSKP---QPQEGNMALESQPQKNKYGHGVFGDVYSII-----------KEMEIDHH
SEQ ID NO:18   LSLSHGAPPV--AREHDGKA-RPAD--DVAHQLAAAGEAGVQKAQKAKKAKKQQLSLRK-
SEQ ID NO:21   LNVCPGVPAGRDPREPDPKVVRAADNCDIAASLAPPFPGSRPPGRRGRGSEEEAAEGRRH
               61                                                     120

            *          *       **    *        * ********   ***
SEQ ID NO:10   NNSTFDFQFPPITNFLGSRE--VREFISGALSGAMTKAILAPLETIRTRMVVG-VGSKNI
SEQ ID NO:18   ------------VRVKIGNPHLRRLVSGAIAGAVSRTFVAPLETIRTHLMVGSSGADSM
SEQ ID NO:21   EEAAAAGRSEPEEGQGQDRQPAPARLVSGAIAGAVSRTFVAPLETIRTHLMVGSIGVDSM
               121                                                    180

            *** *   *** ** **  *  ** ** ***        *        *
SEQ ID NO:10   AGSFIEVIEQQGWQGLWAGNMINMLRIVPTQAIELGTFECVKRAMTSLHEKWESNEYPKL
SEQ ID NO:18   AGVFRWIMRTEGWPGLFRGNAVNVLRVAPSKAIEHFTYDTAKKYLTP----EAGEPAKV
SEQ ID NO:21   AGVFQWIMQNEGWTGLFRGNAVNVLRVAPSKAIEHFTYDTAKKFLTP-----KGDEPPKI
               181                                                    240

            *    ** ** ******    *         *    *   *     *
SEQ ID NO:10   QIGPINFNLSLSWISPVAIAGAAAGIASTLVCHPLEVLKDRLTVSPETYPSLGIAIRNIY
SEQ ID NO:18   PIP--------TPL-VAGALAGVASTLCTYPMELVKTRLTIEKDVYDNLLHAFVKIV
SEQ ID NO:21   PIP--------TPL-VAGALAGFASTLCTYPMELIKTRVTIEKDVYDNVAHAFVKIL
               241                                                    300
```

FIGURE 1B

```
               *  *     *  * * * * * *   **    **        * *      *         *         ****
SEQ ID NO:10   KDGGVGAFYAGISPTLVGMLPYSTCFYFMYDTIKESYCRTKSKKS---LSRPEMLLIGAL
SEQ ID NO:18   RDEGPGELYRGLAPSLLIGVVPYAAANFYAYETLRGVYRRASGK---EEVGNVPTLLIGSA
SEQ ID NO:21   RDEGPSELYRGLTPSLLIGVVPYAACNFYAYETLKRLYRRATGRRPGADVGPVATLLIGSA
301                                                                             360

               **   **     ********     ***     *         *           **     * **  ****** * **  *
SEQ ID NO:10   AGFTASTISFPLEVARKRLMVGALQGKCP-PNMAAALSEVIREEGLKGLYRGWGASCLKV
SEQ ID NO:18   AGAIASTATFPLEVARKQMQVGAVGGRQVYKNVLHAMYCILEKEGTAGLYRGLGPSCIKL
SEQ ID NO:21   AGAIASSATFPLEVARKQMQVGAVGGRQVYQNVLHAIYCILKKEGAGGLYRGLGPSCIKL
361                                                                             420

               **   * ****    **        * *   * **     *
SEQ ID NO:10   MPSSGITWMFYEAWKDILLVQ-----------------NGNPL
SEQ ID NO:18   MPAAGISFMCYEACKKILVDEKEDGGAAEPQEETETGQAGGQAAPKSSNGDRP
SEQ ID NO:21   MPAAGIAFMCYEACKKILVDKEDE-----EEEDEAG--GGEDDKKKVE----
421                                                                             473
```